SEQUENCE LISTING

<110> Commonwealth Scientific and Industrial Reseach Organization

<120> Efficient gene silencing in plants using short dsRNA sequences

<130> BCS-03-2001

<150> US 60/447,711
<151> 2003-02-19

<160> 33

<170> PatentIn version 3.3

<210> 1
<211> 341
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<220>
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       thaliana var. Landsberg erecta

<220>
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<223> XhoI restriction site

<220>
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<222> (7)..(322)
<223> PolIII promoter region

<220>
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<222> (323)..(328)
<223> SalI restriction site

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<222> (329)..(335)
<223> poly T nucleotide stretch

<220>
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<222> (336)..(341)
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<400> 1
ctcgagatgt tgttgttacc agaaagtaaa taaatgttca atctctgatg ttctcaagta   60

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tctcttcttc tatcttaaat ctgtgtatac tatttcacta ttgggctttt tattagtcta   180

taatgggact caaaataagg ctttggccca catcaaaaag ataagtcaca aatcaaaact   240

aaattcagag tcttttctcc cacatcggtc actgtactca ttttgtgttt gtttatatat   300

tacacgaacc gatctttgtt acgtcgactt tttttctcga g   341

<210> 2
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<220>
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      thaliana var. Landsberg erecta including 86 bases downstream of
      the transcription initiation site.

<220>
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<223> XhoI restriction site

<220>
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<222> (7)..(408)
<223> PolIII promoter region.

<220>
<221> misc_feature
<222> (409)..(414)
<223> SalI restriction site

<220>
<221> misc_feature
<222> (415)..(423)
<223> poly T stretch

<220>
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<222> (424)..(429)
<223> XhoI restriction site

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ctcgagatgt tgttgttacc agaaagtaaa taaatgttca atctctgatg ttctcaagta   60

agtgagtttt attgggaata atattaactt atgttcttct tgcatttgat ttctttgccg   120

ctctcttctt ctatcttaaa tctgtgtata ctatttcact attgggcttt ttattagtct   180

ataatgggac tcaaaataag gctttggccc acatcaaaaa gataagtcac aaatcaaaac   240

taaattcaga gtcttttctc ccacatcggt cactgtactc ttttgtgttt gtttatatat   300

tacacgaacc gatctttggt acgtcgagct aagtaacatg agcttgtaac ccatgtgggg   360

acattaagat ggtggaacac tggctcgggt ccacgggccg gttctgttgt cgactttttt   420

tttctcgag   429

<210> 3
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      var. Landsberg erecta

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<223> EcoRI restriction site

<220>
<221> misc_feature
<222> (7)..(313)

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<220>
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<222>   (314)..(319)
<223>   PvuI restriction site

<220>
<221>   misc_feature
<222>   (320)..(328)
<223>   poly T stretch

<220>
<221>   misc_feature
<222>   (329)..(334)
<223>   EcoRI restriction site

<400>   3
gaattcttat gcagcctgtg atggataact gaatcaaaca aatggcgtct gggtttaaga   60

agatctgttt tggctatgtt ggacgaaaca agtgaacttt taggatcaac ttcagtttat   120

atatggagct tatatcgagc aataagataa gtgggctttt tatgtaattt aatgggctat   180

cgtccataga ttcactaata cccatgccca gtaccatgt atgcgtttca tataagctcc   240

taatttctcc cacatcgctc aaatctaaac aaatcttgtt gtatatataa cactgaggga   300

gcaacattgg tcacgatcgt ttttttttga attc   334

<210>   4
<211>   467
<212>   DNA
<213>   Artificial Sequence

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         the transcription initiation site.

<220>
<221>   misc_feature
<222>   (1)..(6)
<223>   EcoRI restriction site

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<222>   (7)..(446)
<223>   Pol III promoter region

<220>
<221>   misc_feature
<222>   (447)..(452)
<223>   XhoI restriction site

<220>
<221>   misc_feature
<222>   (453)..(461)
<223>   poly T stretch

<220>
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<222>   (462)..(467)
<223>   EcoRI restriction site

<400>   4

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agatctgttt tggctatgtt ggacgaaaca agtgaacttt taggatcaac ttcagtttat     120

atatggagct tatatcgagc aataagataa gtgggctttt tatgtaattt aatgggctat     180

cgtccataga ttcactaata cccatgccca gtaccatgt atgcgtttca tataagctcc      240

taatttctcc cacatcgctc aaatctaaac aaatcttgtt gtatatataa cactgaggga     300

gcaacattgg tcacgacctt acttgaacag gatctgttct ataggctcgt acctctgttt     360

ccttgatttc tcaagagaca ggcccttaac cctggttgat gaaccatgac cgtgcggcta     420

gagcgtgatt gacggctacg atcgtcctcg agtttttttt tgaattc                    467


<210>   5
<211>   456
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   sequence of the promoter of the U6-26 snRNA gene of Arabidopsis
        thaliana var. Landsberg erecta including 3 bases downstream of
        the transcription initiation site, followed by a unique
        restriction site in front of an oligo dT stretch


<220>
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<222>   (1)..(6)
<223>   XhoI restriction site

<220>
<221>   misc_feature
<222>   (7)..(436)
<223>   Pol III promoter region

<220>
<221>   misc_feature
<222>   (437)..(442)
<223>   SalI restriction site

<220>
<221>   misc_feature
<222>   (443)..(450)
<223>   poly T stretch

<220>
<221>   misc_feature
<222>   (451)..(456)
<223>   Sac I restriction site

<400>   5
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ttagcttttt ttcttcttct tcgttcatac agtttttttt tgtttatcag cttacatttt     120

cttgaaccgt agctttcgtt ttcttctttt taactttcca ttcggagttt ttgtatcttg     180

tttcatagtt tgtcccagga ttagaatgat taggcatcga accttcaaga atttgattga     240

ataaaacatc ttcattctta agatatgaag ataatcttca aaaggcccct gggaatctga      300

aagaagagaa gcaggcccat ttatatggga aagaacaata gtatttctta tataggccca     360

tttaagttga aaacaatctt caaaagtccc acatcgctta gataagaaaa cgaagctgag     420
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tttatataca gctagagtcg actttttttt gagctc   456

<210> 6
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<212> DNA
<213> Artificial Sequence

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       thaliana var. Landsberg erecta including 20 bases downstream of
       the transcription initiation site, followed by a unique
       restriction site in front of an oligo dT stretch

<220>
<221> misc_feature
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<223> Pol III promoter region

<220>
<221> misc_feature
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<223> PvuI restriction site

<220>
<221> misc_feature
<222> (475)..(482)
<223> Poly T stretch

<220>
<221> misc_feature
<222> (483)..(488)
<223> XhoI restriction site

<400> 6
ctcgagcttc gttgaacaac ggaaactcga cttgccttcc gcacaataca tcatttcttc   60

ttagctttttt ttcttcttct tcgttcatac agttttttttt tgtttatcag cttacattttt   120

cttgaaccgt agctttcgtt ttcttctttt taactttcca ttcggagttt ttgtatcttg   180

tttcatagtt tgtcccagga ttagaatgat taggcatcga accttcaaga atttgattga   240

ataaaacatc ttcattctta agatatgaag ataatcttca aaaggccccct gggaatctga   300

aagaagagaa gcaggcccat ttatatggga aagaacaata gtatttctta tataggccca   360

tttaagttga aaacaatctt caaaagtccc acatcgctta gataagaaaa cgaagctgag   420

tttatataca gctagagtcg aagtagtgat tgtcccttcg gggacatccg atcgttttttt   480

ttctcgag   488

<210> 7
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<212> DNA
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<220>
<223> sequence of the promoter of the U3 snRNA of rice (Oryza sativa

5

Indica IR36)

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<222>  (1)..(6)
<223>  EcoRI restriction site

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<222>  (7)..(384)
<223>  Pol III promoter region

<220>
<221>  misc_feature
<222>  (385)..(390)
<223>  PvuI restriction site

<220>
<221>  misc_feature
<222>  (391)..(399)
<223>  poly T stretch

<220>
<221>  misc_feature
<222>  (400)..(405)
<223>  EcoRI restriction site

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aagttatcag gcatgcatgg atcttggagg aatcagatgt gcagtcaggg accatagcac     120

aggacaggcg tcttctactg gtgctaccag caaatgctgg aagccgggaa cactgggtac     180

gttggaaacc acgtgatgtg gagtaagata aactgtagga gaaaagcatt tcgtagtggg     240

ccatgaagcc tttcaggaca tgtattgcag tatgggccgg cccattacgc aattggacga     300

caacaaagac tagtattagt accacctcgg ctatccacat agatcaaagc tggtttaaaa     360

gagttgtgca gatgatccgt ggcacgatcg tttttttttg aattc                     405
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<210>  8
<211>  442
<212>  DNA
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<220>
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<222>  (1)..(6)
<223>  EcoRI restriction site

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<223>  Pol III promoter region

<220>
<221>  misc_feature
<222>  (422)..(427)
<223>  PvuI restriction site
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<222>   (428)..(436)
<223>   Poly T stretch

<220>
<221>   misc_feature
<222>   (437)..(442)
<223>   EcoRI restriction site

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cattattttc agactctact gaagattgaa ttgaatgaga aactatgaaa ctttacaagt      120

gaattattat ggagttcatg gcaactgcta tggagttttt cctactggga attggaacgg      180

tttctacgaa attaactgtc cacacgttaa aaatataaat taatgcgtaa ttgttatttt      240

ttctataaca aataaaaaac tgaaatacga cataaatttt attactttaa ttgcacttta      300

gccttagaga tattgcgttg tagtcggcgt aggtgtgtca ggggccaata tattgttccc      360

acatcggcag tgcagcacat aaactctagc gttataagaa tctatccact atcaacggtc      420

acgatcgttt tttttgaat tc                                              442
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<210>   9
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<223>   SalI restriction site

<220>
<221>   misc_feature
<222>   (6)..(11)
<223>   PvuI restriction site

<220>
<221>   misc_feature
<222>   (12)..(100)
<223>   GUS sequence (sense)

<220>
<221>   misc_feature
<222>   (101)..(195)
<223>   spacer sequence

<220>
<221>   misc_feature
<222>   (190)..(195)
<223>   BamHI restriction site

<220>
<221>   misc_feature
<222>   (196)..(284)
<223>   GUS sequence (antisense)
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<220>
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<222> (285)..(290)
<223> PvuI restriction site

<220>
<221> misc_feature
<222> (290)..(295)
<223> SalI restriction site

<400> 9
gtcgacgatc gcagcgtaat gctctacacc acgccgaaca cctgggtgga cgatatcacc   60

gtggtgacgc atgtcgcgca agactgtaac cacgcgtctg ttgactggca ggtggtggcc   120

aatggtgatg tcagcgttga actgcgtgat gcggatcaac aggtggttgc aactggacaa   180

ggcactagcg ggatccagac gcgtggttac agtcttgcgc gacatgcgtc accacggtga   240

tatcgtccac ccaggtgttc ggcgtggtgt agagcattac gctgcgatcg tcgac   295

<210> 10
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<212> DNA
<213> Artificial Sequence

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<220>
<221> misc_feature
<222> (1)..(6)
<223> SalI restriction site

<220>
<221> misc_feature
<222> (7)..(42)
<223> GUS sequence (sense)

<220>
<221> misc_feature
<222> (43)..(51)
<223> spacer sequence

<220>
<221> misc_feature
<222> (52)..(87)
<223> GUS sequence (antisense)

<220>
<221> misc_feature
<222> (88)..(93)
<223> Sal I restriction site

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gtcgactggg cagatgaaca tggcatcgtg gtgattgatg aatgcgagaa cttcatcaat   60

caccacgatg ccatgttcat ctgcccagtc gac   93

<210> 11
<211> 50
<212> DNA
<213> Artificial Sequence

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<223> sequence of the dsRNA encoding region of 21 bp for silencing
      expression of the GUS gene (GUShp21)

<220>
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<222> (1)..(6)
<223> SalI restriction site

<220>
<221> misc_feature
<222> (7)..(22)
<223> GUS sequence (sense)

<220>
<221> misc_feature
<222> (23)..(28)
<223> spacer sequence

<220>
<221> misc_feature
<222> (29)..(44)
<223> GUS sequence (antisense)

<220>
<221> misc_feature
<222> (45)..(50)
<223> Sal I restriction site

<400> 11
gtcgactggg cagatgaaca tgtacgatca tgttcatctg cccagtcgac   50

<210> 12
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 42 bp for silencing
      expression of the PHYB gene, derived from the 5' end of PHYB
      (PHYB5hp42)-upper strand

<400> 12
tcgacggagt cgggggtagt ggcggtggcc gtggcggtgg ccgtggagga ggccacggcc   60

accgccacgg ccaccgccac tacccccgac tccg   94

<210> 13
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 42 bp for silencing
      expression of the PHYB gene, derived from the 5' end of PHYB
      (PHYB5hp42)-lower strand

<400> 13
tcgacggagt cgggggtagt ggcggtggcc gtggcggtgg ccgtggcctc ctccacggcc   60

accgccacgg ccaccgccac tacccccgac tccg   94

<210> 14

9

<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 21 bp for silencing
expression of the PHYB gene, derived from the 5' end of PHYB
(PHYB5hp21)-upper strand

<400> 14
tcgacggagt cgggggtagt ggcggaggag gccgccacta cccccgactc cg   52

<210> 15
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 21 bp for silencing
expression of the PHYB gene, derived from the 5' end of PHYB
(PHYB5hp21)-lower strand

<400> 15
tcgacggagt cgggggtagt ggcggcctcc tccgccacta cccccgactc cg   52

<210> 16
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 42 bp for silencing
expression of the PHYB gene, derived from the center of PHYB
(PHYBChp42)-upper strand

<400> 16
tcgatggatg gtgtggttca gccatgtagg gatatggcgg gggaacagga gggttccccc   60

gccatatccc tacatggctg aaccacacca tcca   94

<210> 17
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 42 bp for silencing
expression of the PHYB gene, derived from the center of PHYB
(PHYBChp42)-lower strand

<400> 17
tcgatggatg gtgtggttca gccatgtagg gatatggcgg gggaaccctc ctgttccccc   60

gccatatccc tacatggctg aaccacacca tcca   94

<210> 18
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<212> DNA
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<220>
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expression of the PHYB gene, derived from the center of PHYB
(PHYBChp21)-upper strand

<400> 18
tcgatggatg gtgtggttca gccataggag gatggctgaa ccacacctcc aa   52

<210> 19
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 21 bp for silencing
      expression of the PHYB gene, derived from the center of PHYB
      (PHYBChp21)-lower strand

<400> 19
tcgatggatg gtgtggttca gccatcctcc tatggctgaa ccacaccatc ca   52

<210> 20
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 42 bp for silencing
      expression of the PHYB gene, derived from the 3' end of PHYB
      (PHYB3hp42)-upper strand

<400> 20
tcgacattgt caactgctag tggaagtggt gacatgatgc tgatgaagga ggtcatcagc   60

atcatgtcac cacttccact agcagttgac aatg   94

<210> 21
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 42 bp for silencing
      expression of the PHYB gene, derived from the 3' end of PHYB
      (PHYB3hp42)-lower strand

<400> 21
tcgacattgt caactgctag tggaagtggt gacatgatgc tgatgacctc cttcatcagc   60

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<210> 22
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<212> DNA
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<220>
<223> sequence of the dsRNA encoding region of 21 bp for silencing
      expression of the PHYB gene, derived from the 3' end of PHYB
      (PHYB3hp21)-upper strand

<400> 22
tcgacattgt caactgctag tggaaaggag gttccactag cagttgacaa tg   52

<210> 23
<211> 52
<212> DNA

<220>
<213>   Artificial Sequence

<220>
<223>   sequence of the dsRNA encoding region of 21 bp for silencing
         expression of the PHYB gene, derived from the 3' end of PHYB
         (PHYB3hp21)-lower strand

<400>   23
tcgacattgt caactgctag tggaacctcc tttccactag cagttgacaa tg   52

<210>   24
<211>   94
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   sequence of the dsRNA encoding region of 42 bp for silencing
         expression of the PDS gene (PDS42)-upper strand

<400>   24
tcgacttaac ttgtaaggaa tattacgatc ctaaccggtc aatgctagga ggagcattga   60

ccggttagga tcgtaatatt ccttacaagt taag   94

<210>   25
<211>   94
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   sequence of the dsRNA encoding region of 42 bp for silencing
         expression of the PDS gene (PDS42)-lower strand

<400>   25
tcgacttaac ttgtaaggaa tattacgatc ctaaccggtc aatgctcctc ctagcattga   60

ccggttagga tcgtaatatt ccttacaagt taag   94

<210>   26
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<212>   DNA
<213>   Artificial Sequence

<220>
<223>   sequence of the dsRNA encoding region of 21 bp for silencing
         expression of the PDS gene (PDS21)-upper strand

<400>   26
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<210>   27
<211>   52
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   sequence of the dsRNA encoding region of 21 bp for silencing
         expression of the PDS gene (PDS21)-lower strand

<400>   27
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<210>   28

12

<211> 115
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<223> SalI/PvuI restriction sites

<220>
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<222> (12)..(53)
<223> sense RNA encoding region

<220>
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<222> (54)..(62)
<223> loop structure

<220>
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<222> (63)..(104)
<223> antisense RNA encoding region

<220>
<221> misc_feature
<222> (105)..(115)
<223> SalI/PvuI restriction sites

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gtcgacgatc gtgcggtcac tcattacggc aaagtgtggg tcaataatca ggagttcctt   60

cttcctgatt attgacccac actttgccgt aatgagtgac cgcagtcgac gatcg   115

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<223> sense RNA encoding sequence

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<222> (51)..(59)
<223> loop structure

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<221> misc_feature
<222> (60)..(101)
<223> antisense RNA coding region

13

<220>
<221> misc_feature
<222> (102)..(112)
<223> SalI/pvuI restriction site

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gtcgacgatc gtcatgaaga tgcggacttg cgtggcaaag gattcgataa gttccttctt   60

tatcgaatcc tttgccacgc aagtccgcat cttcatgacg agtcgacgat cg   112

<210> 30
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<213> Artificial sequence

<220>
<223> small hairpin RNA coding region (GUS_C)

<220>
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<223> SalI/PvuI restriction sites

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<223> sense RNA coding region

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<223> antisense RNA encoding region

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